

F4 Another type of mutation which would appear to be of value in improving the thermostability of these  $\alpha$ -amylases is substitution (replacement) of the entire partial amino acid sequence from T369 to I377 (referring to the sequence of *B. licheniformis*  $\alpha$ -amylase; SEQ ID NO: 2) with one of the following partial sequences of six amino acids (sequence numbering increasing from left to right): I-P-T-H-S-V SEQ ID NO: 14); I-P-T-H-G-V SEQ ID NO: 15); and I-P-Q-Y-N-I SEQ ID NO: 16) (or one of the same substitutions of the corresponding partial sequence in *B. amyloliquefaciens*  $\alpha$ -amylase; SEQ ID NO:4).

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F5 Please substitute the filed Sequence Listing with the enclosed substitute Sequence Listing.

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**IN THE CLAIMS:**

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F6 77. (Amended) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to Q298 in *Bacillus licheniformis*.

78. (Amended) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and

thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to G299 in *Bacillus licheniformis*.

79. (Amended) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to G301 in *Bacillus licheniformis*.

80. (Amended) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to Y302 in *Bacillus licheniformis*.

81. (Amended) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to L307 in *Bacillus licheniformis*.

84. (Amended) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to F343 in *Bacillus licheniformis*.

85. (Amended) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to F403 in *Bacillus licheniformis*.

86. (Amended) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to H405 in *Bacillus licheniformis*.

87. (Amended) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said

C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to H406 in *Bacillus licheniformis*.

cont  
F<sub>7</sub>  
88. (Amended) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to D407 in *Bacillus licheniformis*.

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F<sub>8</sub>  
90. (Amended) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to L427 in *Bacillus licheniformis*.

91. (Amended) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and

thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to I428 in *Bacillus licheniformis*.

F<sub>8</sub>  
92. (Amended) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to D430 in *Bacillus licheniformis*.

93. (Amended) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to G433 in *Bacillus licheniformis*.

F<sub>9</sub>  
97. (Amended) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to G475 in *Bacillus licheniformis*.

~~Def G1~~  
~~F10~~  
113. (Amended) An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to one or more of Q298, G299, G301, Y302, L307, F343, F403, H405, H406, D407, L427, I428, D430, G433, and G475 in *Bacillus licheniformis* (SEQ ID NO:2).

~~Def G2~~  
~~F11~~  
118. (Amended) The alpha-amylase according to claim 113, wherein said alpha- amylase further comprises a substitution or deletion at one or more residues equivalent to M15, N188, A209 and/or M197 in *Bacillus licheniformis* (SEQ ID NO:2).

119. (Amended) The alpha-amylase according to claim 113, wherein said alpha-amylase comprises a substitution ~~or~~ deletion at one or more residues equivalent to M15, N188, A209, and/or M197 in *Bacillus licheniformis*.

120. (Amended) The alpha-amylase according to claim 113 which is modified by substituting an amino acid residue at a position corresponding to one or more of G301, H405 and/or H406 in *Bacillus licheniformis*.

121. (Amended) An alpha-amylase ~~comprising~~ comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said

F<sub>11</sub>  
C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to one or more of Q298, G299, G301, Y302, L307, F343, H405, H406, D407, I428, D430, and G475 in *Bacillus licheniformis* (SEQ ID NO:2).

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Def G3  
F<sub>12</sub>  
126. (Amended) The alpha-amylase according to claim 121, wherein said alpha-amylase further comprises a substitution or deletion at one or more residues equivalent to M15, N188, A209 and/or M197 in *Bacillus licheniformis* (SEQ ID NO:2).

127. (Amended) The alpha-amylase according to claim 121, wherein said alpha-amylase further comprises a substitution or deletion at one or more residues equivalent to M15, N188, A209, and/or M197 in *Bacillus licheniformis* (SEQ ID NO:2).

128. (Amended) A variant of a parent alpha-amylase,  
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and  
wherein, in said variant, at least one amino acid residue at a position corresponding to one or more of, Q298, G299, G301, Y302, L307, F343, F403, H405, H406, D407, L427, I428, D430, G433, and G475 in *Bacillus licheniformis* (SEQ ID NO:2) has been substituted.

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F13  
133. (Amended) The variant according to claim 128, wherein said variant further comprises a substitution or deletion at one or more residues equivalent to M15, N188, A209 and/or M197 in *Bacillus licheniformis* (SEQ ID NO:2).

134. (Amended) The variant according to claim 128, wherein said variant further comprises a substitution or deletion at one or more residue equivalent to M15, N188, A209, and/or M197 in *Bacillus licheniformis* (SEQ ID NO:2).

135. (Amended) The variant according to claim 128, wherein said variant comprises a substitution at an amino acid residue at a position corresponding to one or more of G301, H405 and/or H406 in *Bacillus licheniformis* (SEQ ID NO:2).

136. (Amended) A variant of a parent alpha-amylase,  
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and

wherein, in said variant, at least one amino acid residue at a position corresponding to one or more of Q298, G299, G301, Y302, L307, F343, H405, H406, D407, I428, D430, and G475 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.



141. (Amended) The variant according to claim 136, wherein said variant further comprises a substitution or deletion at one or more residues equivalent to M15, N188, A209 and/or M197 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2).

F<sub>14</sub>  
142. (Amended) The variant according to claim 136, wherein said variant further comprises a substitution or deletion at one or more residues equivalent to M15, V128, H133, N188, A209, and/or M197 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2).

143. (Amended) A variant of a parent alpha-amylase,  
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and  
wherein, in said variant, the amino acid residue at a position corresponding to Q298 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

144. (Amended) A variant of a parent alpha-amylase,  
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and  
wherein, in said variant, the amino acid residue at a position corresponding to G299 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

145. (Amended) A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and

wherein, in said variant, the amino acid residue at a position corresponding to G301 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

146. (Amended) A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and

wherein, in said variant, the amino acid residue at a position corresponding to Y302 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

147. (Amended) A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and

wherein, in said variant, the amino acid residue at a position corresponding to L307 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

148. (Amended) A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and

wherein, in said variant, the amino acid residue at a position corresponding to F343 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

149. (Amended) A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and

wherein, in said variant, the amino acid residue at a position corresponding to F403 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

150. (Amended) A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and

wherein, in said variant, the amino acid residue at a position corresponding to H405 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

151. (Amended) A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and

wherein, in said variant, the amino acid residue at a position corresponding to H406 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

152. (Amended) A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and

wherein, in said variant, the amino acid residue at a position corresponding to D407 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

153. (Amended) A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and

wherein, in said variant, the amino acid residue at a position corresponding to L427 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

154. (Amended) A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and

wherein, in said variant, the amino acid residue at a position corresponding to I428 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) which has been substituted.

155. (Amended) A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and

wherein, in said variant, the amino acid residue at a position corresponding to D430 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

156. (Amended) A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and

wherein, in said variant, the amino acid residue at a position corresponding to G433 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

157. (Amended) A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and

wherein, in said variant, the amino acid residue at a position corresponding to G475 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

158. (Amended) A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, and

wherein, in said variant, at least one amino acid residue at a position corresponding to one or more of, Q298, G299, G301, Y302, L307, F343, F403, H405, H406, D407, L427, I428, D430, G433, and G475 in *Bacillus licheniformis* (SEQ ID NO:2) has been substituted.

163. (Amended) The variant according to claim 158, wherein said variant further comprises a substitution or deletion at one or more residues equivalent to M15, N188, A209 and/or M197 in *Bacillus licheniformis* (SEQ ID NO:2).

164. (Amended) The variant according to claim 158, wherein said variant further comprises a substitution or deletion at one or more residue equivalent to M15, N188, A209, and/or M197 in *Bacillus licheniformis* (SEQ ID NO:2).

165. (Amended) The variant according to claim 158, wherein said variant [further] comprises a substitution at an amino acid residue at a position corresponding to one or more of G301 and/or H405 in *Bacillus licheniformis* (SEQ ID NO:2).

F<sub>15</sub>  
166. (Amended) A variant of a parent alpha-amylase,  
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:  
2, 4, 6, or 13, and

wherein, in said variant, at least one amino acid residue at a position corresponding to one or more of Q298, G299, G301, Y302, L307, F343, H405, H406, D407, I428, D430, and G475 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

F<sub>16</sub>  
171. (Amended) The variant according to claim 166, wherein said variant further comprises a substitution or deletion at one or more residues equivalent to M15, N188, A209 and/or M197 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2).

172. (Amended) The variant according to claim 166, wherein said variant further comprises a substitution or deletion at one or more residues equivalent to M15, [V128, H133,] N188, A209, and/or M197 in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2).

173. (Amended) A variant of a parent alpha-amylase,  
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:  
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to Q298  
in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

FIG 174. (Amended) A variant of a parent alpha-amylase,  
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:  
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to G299  
in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

175. (Amended) A variant of a parent alpha-amylase,  
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:  
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to G301  
in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

176. (Amended) A variant of a parent alpha-amylase,  
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:  
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to Y302  
in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.



177. (Amended) A variant of a parent alpha-amylase,  
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:  
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to L307  
in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

178. (Amended) A variant of a parent alpha-amylase,  
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:  
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to F343  
in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

179. (Amended) A variant of a parent alpha-amylase,  
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:  
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to F403  
in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

180. (Amended) A variant of a parent alpha-amylase,  
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:  
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to H405  
in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

181. (Amended) A variant of a parent alpha-amylase,  
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:

2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to H406  
in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

182. (Amended) A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:  
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to D407  
in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

183. (Amended) A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:  
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to L427  
in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

184. (Amended) A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:  
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to I428  
in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) which has been substituted.

185. (Amended) A variant of a parent alpha-amylase,  
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:

2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to D430  
in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

186. (Amended) A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:  
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to G433  
in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

187. (Amended) A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:  
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to G475  
in *Bacillus licheniformis* alpha-amylase (SEQ ID NO:2) has been substituted.

193. (Amended) A variant of a parent alpha-amylase, said variant having an amino acid sequence which differs from the amino acid sequence of said parent, wherein the difference between said variant and said parent comprises a different amino acid residue in said variant than in said parent at one or more positions selected from the group consisting of the positions which correspond to amino acid residues Q298, G299, G301,